Supplementary Information

The ankyrin repeat domain of Huntingtin interacting protein 14 contains a surface aromatic cage, a potential site for methyl-lysine binding

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Submit to *Proteins: Structure, Function, and Bioinformatics* as a Structure Note

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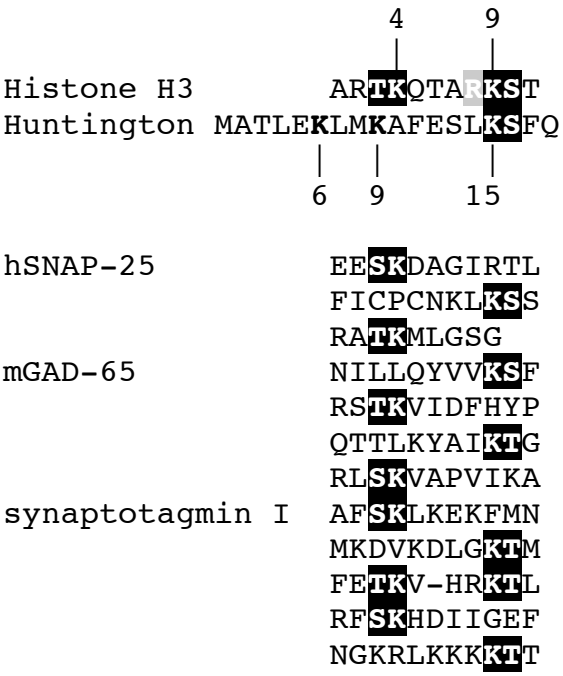
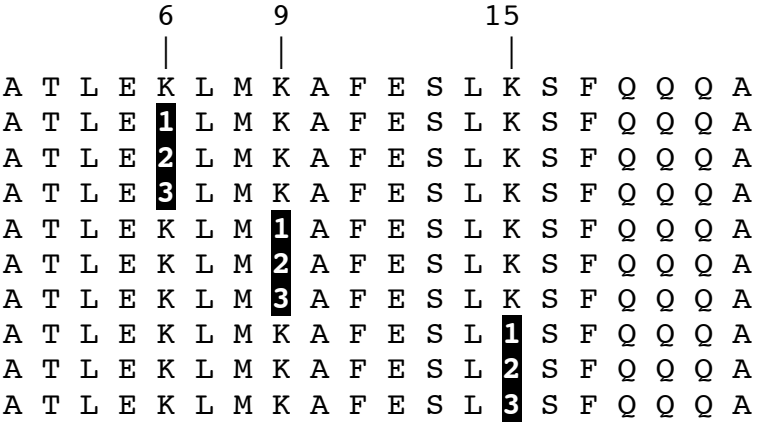
Supplementary Table 1. HIP14 substrates contain sequence(s) similar to histone H3 tail sequence



Supplementary Table 2. Methylated Huntingtin peptides used in the study



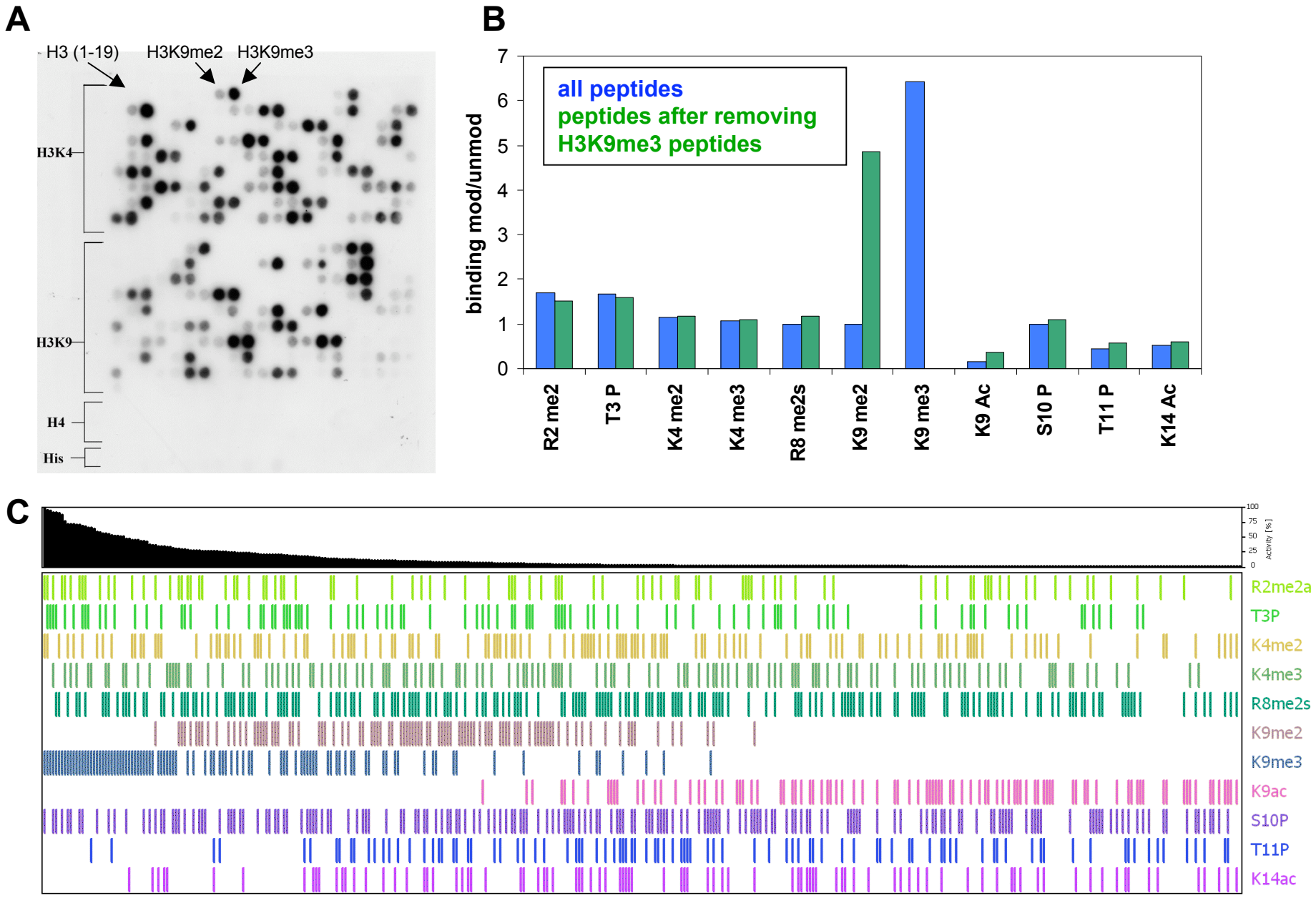
1: Kme1 - monomethyl lysine
2: Kme2 - dimethyl lysine
3: Kme3 - trimethyl lysine

Supplementary Figure 1. Binding of HP1ß chromodomain to peptide arrays

(A) Example of HP1ß binding to peptide arrays containing histone tail peptides containing different combinations of post translational modifications.

(B) Average of the binding intensities to all spots containing a particular modification divided by the binding to all spots not containing this modification. The data show a strong preference for binding to H3K9me3 (blue bars). After disregarding all H3K9me3 peptides, the analysis indicated that binding to H3K9me2 is the second next preference.

(C) Histogram of all peptide sequences present on the array. The peptides were sorted by binding intensity and the presence of some of the post translational modifications indicated.


A
H3 (1-19)
H3K9me2
H3K9me3
H3K4
H3K9
H4
His
B
all peptides
peptides after removing
H3K9me3 peptides
binding mod/unmod
0
1
2
3
4
5
6
7
R2 me2
T3 P
K4 me2
K4 me3
R8 me2s
K9 me2
K9 me3
K9 Ac
S10 P
T11 P
K14 Ac
C
100
75
50
25
0
Activity [%]
R2me2a
T3P
K4me2
K4me3
R8me2s
K9me2
K9me3
K9ac
S10P
T11P
K14ac